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OIPF

#17

RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/749,185

TIME: 11:36:05

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3 <110> APPLICANT: van Wezel, Gilles
 4 Kraal, Barend
 5 Luiten, Rudolf
 7 <120> TITLE OF INVENTION: REDUCING BRANCHING AND ENHANCING FRAGMENTATION IN CULTURING
 FILAMENTOUS
 8 MICROORGANISMS
 10 <130> FILE REFERENCE: 2183-4666US
 12 <140> CURRENT APPLICATION NUMBER: US 09/749,185
 13 <141> CURRENT FILING DATE: 2000-12-26
 15 <150> PRIOR APPLICATION NUMBER: EP 98202148.7
 16 <151> PRIOR FILING DATE: 1998-06-26
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 438
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Streptomyces griseus
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 32 ttccaccttc ccggcgatgc cctgtgacc tgggcgttcg gccgcgagct gctgctggac 180
 34 gggctcaaca gcccgagcgg cgacggcgat gtgcacatcg gcccgaccga gcccgagggc 240
 36 ctccggagatg tccacatccg gctccaggtc ggcgcggacc gtgcgctgtt ccgggcgggg 300
 38 acggcaccgc tgggtggcgtt cctcgaccgg acggacaagc tcgtgccgct ccggcaggag 360
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 52 <222> LOCATION: (1)..(405)
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 57 1 5 10 15
 59 ctc cga tac gag gtc ggc gat ccg tat gcc atc cgg atg acg ttc cac 96
 60 Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His
 61 20 25 30
 63 ctt ccc ggc gat gcc cct gtg acc tgg gcg ttc ggc cgc gag ctg ctg 144
 64 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
 65 35 40 45
 67 ctg gac ggg ctc aac agc ccg agc ggc gac ggc gat gtg cac atc ggc 192
 68 Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly
 69 50 55 60
 71 ccg acc gag ccc gag ggc ctc gga gat gtc cac atc cgg ctc cag gtc 240
 72 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val

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75 ggc gcg gac cgt gcg ctg ttc cgg gcg ggg acg gca ccg ctg gtg gcg      288
76 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala
77          85          90          95
79 ttc ctc gac cgg acg gac aag ctc gtg ccg ctc ggc cag gag cac acg      336
80 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr
81          100          105          110
83 ctg ggt gac ttc gac ggc aac ctg gag gac gca ctg ggc cgc atc ctc      384
84 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu
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103 Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His
104          20          25          30
107 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
108          35          40          45
111 Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly
112          50          55          60
115 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val
116 65          70          75          80
119 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala
120          85          90          95
123 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr
124          100          105          110
127 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu
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131 Ala Glu Glu Gln Asn Ala Gly
132          130          135
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136 <211> LENGTH: 407
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138 <213> ORGANISM: Streptomyces albus G
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147 1          5          10          15
149 ctg cgg tac gag acc gtc gat ccg tac gcg gtg cgg ctg acg ttc cac      96
150 Leu Arg Tyr Glu Thr Val Asp Pro Tyr Ala Val Arg Leu Thr Phe His

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153 ctc ccc gga gac gcc ccg gtc acc tgg gtc ttc ggg cgt gaa ctg ctg      144
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155          35          40          45
157 gtc gag gga gtc ctg gac gcc gcg ggc gac ggc gac gtc cgg gtc tgc      192
158 Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys
159          50          55          60
161 ccg gtg ggg cag acg gcc acc agg gag gtg cac atc acc ctc cag gtc      240
162 Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val
163 65          70          75          80
165 ggc tcc gag cag gcg ctc ttc cgc gtc ggc aag gcg ccg ctg ctc gcc      288
166 Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala
167          85          90          95
169 ttc ctc gac cgc acc gac cag ggc ttg tcg ctc ggc agc gag cgg gca      336
170 Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala
171          100          105          110
173 cac gcc gac ttc gac agc cac ctc gac gac gct ctg aac cgc agc ctc      384
174 His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu
175          115          120          125
177 gcc gag gag cag agc gcc ggc tg      407
178 Ala Glu Glu Gln Ser Ala Gly
179          130          135
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183 <211> LENGTH: 135
184 <212> TYPE: PRT
185 <213> ORGANISM: Streptomyces albus G
187 <400> SEQUENCE: 5
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190 1          5          10          15
193 Leu Arg Tyr Glu Thr Val Asp Pro Tyr Ala Val Arg Leu Thr Phe His
194          20          25          30
197 Leu Pro Gly Asp Ala Pro Val Thr Trp Val Phe Gly Arg Glu Leu Leu
198          35          40          45
201 Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys
202          50          55          60
205 Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val
206 65          70          75          80
209 Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala
210          85          90          95
213 Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala
214          100          105          110
217 His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu
218          115          120          125
221 Ala Glu Glu Gln Ser Ala Gly
222          130          135
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 407
227 <212> TYPE: DNA
228 <213> ORGANISM: Streptomyces goldeniensis

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237 1          5          10          15
239 ctg cgt tac gag acc tgt gat ccc tac gcc gtg cgg ctg acc ttt cat      96
240 Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His
241          20          25          30
243 ctg ccc gga gat gcc ccg gtg acc tgg gcg ttc ggg cgg gag ttg ctc      144
244 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
245          35          40          45
247 atc gac gga ggt ccg cgg ccg tgc ggg gac ggg gac gtc cac atc gcg      192
248 Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala
249          50          55          60
251 ccc gcc gac ccg gag acg ttc ggc gag gtc ctg atc cgc ctg cag gtg      240
252 Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val
253 65          70          75          80
255 ggg agc gac cag gcg atg ttc cgg gtc ggc acg gcg ccg ctg gtg gcc      288
256 Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala
257          85          90          95
259 ttc ctg gac cgc acg gac aag atc gtg ccg ctg ggg cag gag cgt tcc      336
260 Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser
261          100          105          110
263 ctc gcc gac ttc gac gcc ctg ctc gac gag gcg ctg gac cgc atc ctg      384
264 Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu
265          115          120          125
267 gcc gag gag cag aac gcc ggc'tg      407
268 Ala Glu Glu Gln Asn Ala Gly
269          130          135
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275 <213> ORGANISM: Streptomyces goldeniensis
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283 Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His
284          20          25          30
287 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
288          35          40          45
291 Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala
292          50          55          60
295 Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val
296 65          70          75          80
299 Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala
300          85          90          95
303 Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser

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304          100          105          110
307 Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu
308          115          120          125
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312          130          135
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318 <213> ORGANISM: Streptomyces netropsis
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322 <222> LOCATION: (1)..(405)
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327 1          5          10          15
329 ctg cga tac gag acc cgg gat ccc tac gcg gtg cgg atg acc ttc cac      96
330 Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His
331          20          25          30
333 ctc ccc gga gac gcg cct gtg acc tgg gcg ttc ggc cgg gag ctg ctg      144
334 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
335          35          40          45
337 ctc gac ggg atc aac cgc ccg agc ggc gac ggc gac gtc cac atc gcc      192
338 Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala
339          50          55          60
341 ccg acc gac ccc gag ggc ctg tcg gac gtc tcc atc cgg ctc cag gtg      240
342 Pro Thr Asp Pro Glu Gly Leu Ser Asp Val Ser Ile Arg Leu Gln Val
343 65          70          75          80
345 ggc gcg gac cgc gcc ctc ttc cgt gca ggc gcc ccg ccg ctg gtc gcc      288
346 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala
347          85          90          95
349 ttc ctc gac cgc acg gac aag tcg gtg ccg ctc ggt cag gaa cag act      336
350 Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr
351          100          105          110
353 ctg ggt gac ttc gag gac agc ctg gag gcc gcg ctc ggc aag atc ctc      384
354 Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu
355          115          120          125
357 gcc gag gag cag aac gcc ggc tg      407
358 Ala Glu Glu Gln Asn Ala Gly
359          130          135
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364 <212> TYPE: PRT
365 <213> ORGANISM: Streptomyces netropsis
367 <400> SEQUENCE: 9
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373 Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/749,185

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